30.APR.2002 18:07 eadoy, 30 April 2002

IOCHEMISTRY 643 479 7866

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results of BLAST

TBLASTN 2.2.3 [Apr-24-2002]

ARMACRASE!
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Alejandro A. Schäffer,
Binghui Zhang, Zhang, Webb Miller, and David J. Lipman (1997),
Schped BLAST and PSI-BLAST: a new generation of protoin database search
programs, Nucleic Acids Red. 25:3389-3402.

RID: 1020140625-011436-28352

Query

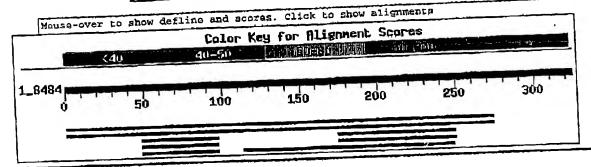
(324 lotcers)

Database: All GenBank+EMBL+DDEJ+PDB sequences (but no BST, STS, GSS, or phase 0, 1 or 2 HTGS sequences) 1,218,445 sequencos; 5,427,962,278 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FADE

Taxonomy reports

Distribution of 9 Blast Hits on the Query Sequence



Aligaments

| | Score | E | |
|--|--------|-------|-------------|
| | (bits) | Value | |
| Sequences producing significant alignments: | • | | |
| | 549 | g-154 | |
| 01 2536718 gh AF007776 1 AF007776 Candida albicans Chromoso | 549 | e-154 | |
| gi 3273716 gh AF050216.1 AF050216 Candida albicana chromess | 40 | 0.30 | |
| rd 3273716 oh AF050216 1 AF050210 talidate olegans cosmid P47D | | | L |
| described the elegans | _40 | 0.30 | _ |
| gill7553483 ref NM 065980 1 Caenorhabditis elegans | _32 | 4.1 | arest staff |
| 24 20197371 Job AC005397.31 AFSP100PH10 200 | _35 | 9.7 | EU |
| 91 1754514 501 D87515 1 D87515 Rattus norvegicus mRNA for a | | | ΨÜ |
| 93 11/24/17/19/19 | _35 | 9.7 | |
| gill3592046 ref NM 031097.1 Rattus norvegicus eminopeptide | | | 1 L |
| | _35 | 9.7 | 100 |
| gi 2039142 ab u61696.1 RNU61696 Rattus norvegicus aminopent | | | |

>g1|2636718|c5|AF007776.1|AF007776 Candida albicans Length c 6426

Score = 649 bits (1415), Expect = 0-154 Identities = 272/274 (99%), Positives = 272/274 (99%)

| Frame | = | | |
|--------|---|--|---|
| | | FIRE THE PROPERTY OF THE PROPE | |
| QUETY: | 1 | mssakndinegrvmesvdoanaiskudrhikarfmmlfikfndlpklavgnorsvokmne Mssakndinegrvmesvdoanaiskudphikarfmmlfikfndlpklavgnorsvokmne Mssakndinegrvmesvdoanaiskudphikarfmmlfikfndlpklavgnorsvokes 57 | |
| | | MESAKNDDNEGKVMESVDQANAIBKVUERIKARENNILL III DEL AVGNOK TVDKWNE S7 | 7 |

Sbjct: 398 MSSAKNDDNEGKVMESVDQANAISKVDBHIKARFNMLFIKFNDLPKLAVGNQKSVDKWNE 577

Query: 61 EFKYPHVAYPDVLEFLLDYNPKDKPKVKVEGIYPTGWCLQMCLQSIFDRFRLIMISKLP 120 PFKYPHVAYPDVLEFLLDYNFKDKFKVKKVEGIYFTGWCLQMCLQSIFDRFRLIMISKLF

Sbjct: 578 EFKYFHVAYPDVLEFLLDYNPKDKPKVKKVEGIYFTGWCLQMCLQSIFDRFRLIMISKLP 757

Query: 121 KHLQKEANLIKAAYDAVUKSKDYTITSKILSKFVNVEHELVVCYNLFYLSQVEEKLEEIL 180 KHLQKEANLIKAAYDAVUKSKDYTITSKIL KFVNVEHELVVCYNLFYL QVEEKLEEIL

Sbjot: 758 KHLQKEANLIKAAYDAVTKSKDYTITSKILLKFVNVEHELVVCYNLPYLLQVEEKLEEIL 937

Query: 181 Yntsnvvdeyvrslpnliggvlyfnhvkksealslflmihagyyskwigadndtsvlpsc 240 ANIENAADEAAKSTBUTIEGATAANAAKKEEYTETETHYVEAKAIOVDUTEATBEC

Received Time 30.Apr. 18:38 Phylodolegical District Control of the Control of the

NO.387

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30 APR 2002 18:07 SDJCC: 938 YNTSNVVDEYVRSLENLIGQVLYO U BIOCHEMISTRYYYSKWIQADNDTSVLPSC 1117

Query: 241 STIARPMCDHPDYARLVDIPSNKYELNLIVSLPA 274

STIAEEMCDHPDYARLVDIPSNKYELNLIVSLPA Sbjct: 1118STIAEEMCDHPDYARLVDIPSNKYELNLIVSLPA 1219

>31/3273716 ab AFR50215. 1 AFR50215 Candida albicans chromosome 3 map between CDR1 and DYN1 Strain nog759

Length = 6980

Score = 549 bits (1415), Expect = q-154 Identities = 272/274 (99%), Positivos = 272/274 (99%)

MSSAJONDDNEGKVMESVDQANAISKVDEMIRARFNMLFIRFNDLPRLAVGNQKSVDKWME 60 Frame = +1 wssaknddnbgkvmesydoanaiskydehikarfnmlfikfndlfrlavgnoksydkynb EDJCC: 604 MSSAKNDDNEGKVMESVDQANAISKVDEHIKARFNMLFIKFNDLPKLAVGNQKSVDKWNE 783 Query: 1

Query: 61 EFKYFHVAYPDVLHFLLDYNFKDKFKVKKVEGIYFTGWCLQMCLQSIFDRFRLINISKLP 120

Sbjet: 784 EFKYFHVAYPDVLEFLLDYNPKDKFKVKKVEGIYFTGWCLQMCLQSIFDRFRLIMISKLP 963

QUETY: 121 KHLOKEANLIKANYDAVTKSKDYTITSKILSKPVNVEMBLVVCYNLFYLSQVEEKLEEIL 180 KHLOKEANLIKANYDAVTKSKDYTITSKIL KFVNVEHELVVCYNLFYL QVEEKLEEIL Sbjet: 964 KHLQKEANLIKAAYDAVTKSKDYTITSKILLKFVNVEHBLVVCYNLBYLLQVBEKLEEIL 1143

Quory: 181 Yntsnvvdeyvrslpnligqvlyfnhvkksealslplnihasyyskwiqadndtsvlpsc 240 Yntenvvdeyvrslpnligqvlyfnhvkksbalslplnihasyyskwiqadndtsvlpsc

Sbjct: 1144YNTSNVVDEYVRSLPNLIGQVLYFNHVKKSEALSLFINIHASYYSKWIQADNDTSVLPSC 1323

Query: 241 STIAREMCDHPDYARLVDIPSNKYELNLIVSLPA 274 STIAEEMCOHPDYARLVDIPSNKYBLNLIVELPA Sbjc: 1324STIAEEMCDHPDYARLVDIPSNKYELNLIVSLPA 1425

>g1 | 13366236 | qb | U22631 21 | Caenorhabditis elogans cosmid F47D12, complete sequence Longth = 42275

Scora = 40.0 bits (92), Expost = 0.30 Identities = 24/80 (30%), Positives = 36/80 (45%), Gaps = 4/80 (5%) Prame = -1

KLEBILYNTENVVDEYVRALE----NLIGOVLYFNHVKKSEALSLPLNIHASYYSKWIQA 230 K I N + +D S+P NL + YFNH+ K + + TH S+Y WI Sbjec: 18740 KKNSISINIDSKLDHIWGSIPLNBBNLYCCIRYFNHIPKIRBTGCW--IHKBFYLNWIHE 18567

DNDTSVLPSCSTIARENCOH 250 Query: 231 + VP T+ ++ DH Sbjer: 18566 STNKKVKPCVLTVRROLVDN 18507

>gi|17553483|ref|NM 065980]| Caenorhabditis elegans Length = 423

Schre = 40.0 bits (92), Export = 0.30 Identities = 24/80 (30%), Posttives = 36/80 (45%), Gaps = 4/80 (5%)

Query: 175 KLEBILYNTSNVVDEYVRSLB----NLIGOVLYFNHVKKBEALSLFLNIHASYYSKWIQA 230 NL + YENH+ K + Sbjct: 234 KKNSISINIDEKLDWINGSIPLNSENLYCCIRYENHIPKIRSTGCW--THKSFYLNWIHF 61

Query: 231 DNDTSVLPSCSTIABEMEDH 250 V P T)+ Sbjec: 60 STNKKVKPCVLTVERQLVDH 1

>ELI 20197371 ED ACO05397 31 Arabidopsis thaliana chromosoms 2 clone T3F17 map CIC02E07, complete sognance Length = 110149

Score = 32.0 bits (71), Expect(2) = 4.1 Identities = 25/120 (20%), Positivas = 60/120 (69%), Gaps = 4/120 (3%)

IMISKLPKHLQKEANLIKAAYDAUTKEKDYTITSKILSKFVNVEHELVVCYNLPYLEQVE 173 I++ L K L K ++ Y ++S+ T T++++S +V++ T+ + +S ++

Sbjc: 48288 ILMQLLVKGL-KLLTMVATIY-RIYQSRSITTTEVISTWVDLLR*VLCKSPIBSISYLK 48464 Query: 114

EKLEBILYNTSNYVDEYVRSLENLIGQVLYFNHVKKSEALSLFLDIHASYYSK----WIO 229 6bjct: 48465 EVIQLV--- BGNIDQKRMGCISECRRKVSYQNNIS* FEAFDVLLNVLMSIYSRIPGHWVQ 48635

Score = 22.7 bits (47), Expect(2) = 4.1 Identities = 7/17 (41%). Positives = 12/17 (70%) Frame = +1

DTSVLPSCSTIAEEMCD 249 Query: 233 D+ +L SC+T+ Sbjec: 48715 DERILVSCNTLYSRLOD 48765

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Length = 2192

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>91/1754514 | Abi | D97515 1 | D97515 | Rectus norvegicus mana for aminopeptidase-B. complete cds

Score = 35.0 bits (79), Expect = 9.7 Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%) Frame = +3

AGUŐKBADK----MUEELKÁŁHAVABDAFBEFFFDANBKDKŁK-AKKARGIAŁLOM BB + +EFK+ + D LEF L+Y P+ K K V + G F Query: 49 SDJCL: 1284 VGDQEQFDKFLKAYVDEFKFQSILAEDFLEFYLEYFPBLKKKGVDSIFGFEFNRW 1448

>gi|13592046|ref|NM 031097.1| LU Rattus norvegicus aminopeptidase B (Rnpep), mRNA Length = 2208

Score = 35.0 bits (79). Expect = 9.7 Identicies = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%) Frame = +3

VCNOKSUDK----WNEEPKYPHVAYPDVLBPLLDYNPKDKFK-VKKVEGIYFTGW 98 VG+Q+ DK · + +BFK+ + D LEF L+Y P+ K K V + G F W

Sbjct: 1287 VGDQEQFDKFLKAYVDEFKFQSILAEDFLEFYLEYFPELKKKGVDSIPGFEFNRW 1451

Length = 2208

Score = 35.0 bits (79), Expect = 9.7 Identitics = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%) Framo = +3

VGNQKSVDK----WNEEFKYFHVAYPDVLEFLLDYNPKDKFK-VICKVEGIYFTGW 98 VG+Q+ DK + +EFK+ + D LEF L+Y P+ K K V + G F W Query: 49 SDjct: 1287 VQDQEQFDKFLKAYVDEFKFQSILAEDFLEFYLEYFFELKKKGVDSIFQFEFNRW 1451

Databage: All GenBank+EMBL+DDBJ+PDB acquences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
or phase 0, 1 or 2 HTGS sequences)
Posted date: Apr 29, 2002 1:59 AM
Number of letters in database: 1,132,994,982 Number of sequences in database: 1,218,445

abdme,1 K H 0.368 0.317

Gapped **Abdmed** 0.140 0.267 0.0410

Matrix: BLOSUM62 Gap Ponalties: Existence: 11. Extension: 1 Number of Hits to DB: 1,648,687,762 Number of Sequences: 1218445 Number of extensions: 24413213 Number of successful extensions: 103318
Number of successful extensions: 103318
Number of sequences better than 10.0; 16
Number of HSP's better than 10.0 without gapping: 38293
Number of HSP's better than 10.0 without gapping: 38293 Number of MSP's successfully gapped in prelim test: 5836 Number of MSP's that attempted gapping in prelim test: 52250 Number of MSP's gapped (non-prelim): 69771 length of query: 324 length of database: 1,809,320,759 effective HSP length; 136 effective length of quory: 188 offective length of database: 1.642,612.239 effective search space: 308999100932 effective soarch space used: 308989100932 frameshift window, decay const: 50, 0.1 T: 13 A; 40 X1: 16 (7.3 bita) X2: 38 (14.6 bits) X3: 64 (24.7 bits) 91: 41 (21.7 bits) S2: 79 (35.0 bits)

78E.0N

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Related Sequences, Protein, Taxonomy

1: AF050215. Candida albicans ...[gi:3273716]

AFOSO213 SHEU DD DNA IIRGI FMW UI-UD-1996 Candida albicana Teal retrotransposon gas polyprotein (gas) and pol polyprotein (pol) genes, complete cds. lineas LOCUS DEFINITION

AF050215 ACCESSION VERSION KEYWORDS

AF050215.1 QI:3273716

candida albicans. SOURCE ORGANISM

Candida Albicana Candida Albicana Eukaryota; Pungi; Ascomycota; Saccharonycacalos; Candida. Sucharomydetales; mitosporic Saccharomydetales; Candida. 1 (bages 1 to 5980) Goodwin, T.J.D. and Poultor, R.T.M. Tomperature- and strain-dependent expression of the pCal rotternsposen of Candida albiens

REFERENCE

AUTHORS rotrotransposon of Candida albicans TITLE

Unpublished TOURNAL (bases 1 to 6980) REFERENCE

Goodwin.T.J.D. and Poulter, R.T.M. AUTHORS

TITLE JOURNAL

Submitted (20-FEB-1998) Department of Bischemiatry, University of Ottom (20-FEB-1998) Department of Ottom (20-FEB-1998) Department of Ottom (20-FEB-1998) Department of Ottom (20-FEB-1998) Department of Ottom (20-FEB-1998) De

FEATURES DOUTCE . 6980

/organism="Candida albicans" /strain="hoc789"

/db_xrof="taxon:5476" /usba.perwoon CDMI and DANI

202.,206 misc frature /norse=3. carder site doblications 207..6632 /rpt_familys Tra2 retrocransposon rangak region

/rpt_cypaudispersed /note==5' long terminal repeat' LTB

/noces'complements can's Arg(UCU) fragmonts 604.1578 primer hind

9000 /gone='gag 604.,1578 CDS /genes 'gag /coden_starte1

/guada_praired /rransl_table=12 /product=*gap polyprotein* /protein_id=*AACAGE20_1* /db_wof=*GI:3273717*

/Etanslbeiond masakniddnegkvmesvidanaiskvidhikarfmalfikfnil Pklavenokevidroneefkyfhvayfdvleflidtnerdkfkvakvegiyftgwclom CLQSIFORFRLIMISKLPRHLQKEANLIKAAYDAVTKBKDYTITSKILSKTVNVEHEL CTGSIFDRERITIMISKLPKHIQKEANIKH PRSDNDKGEKEKEKISSE.

THYBAA ZKMIGYDNDÆRITIKERANANEH BRZDNDKERKEKIRISSE.

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KÖKÖKBERISERITIKERANTIKYYADYALRENDALIZKTISKLANANGHEF.

misc feature

1576..1578 /gene='gag" /nouse potentially suppressed stop coden'

<1579. 6309 GODO /gone="pol <1579..6309 CDS

/geno=*pol* /notes*included professe, integrase, reverce transcriptase, RNage H*

/codon_start=1 /crunsl_table=12 /product="pol polyprotein" /protein_id="AAC24821.1" /db_xref="GI:3273718"

/Drocein_id="AAC2dB21.1"
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KXLVYDTAATISVVNNKDILSNVKDATIEVEVADQATLBADDIGDLIIRVGTVSITTE
FSEESLECDPDYDGLADMLSNANDDDKDKSSMASSEYQEHDYSSFALINSITEVDVDV
BSEESLECDPDYDGLADMLSNANDDDKDKSSMASHSEYQEHDYSSFALINSITEVDVDV
DCKVCLLSNAKQRSKMHHSERKASRAHERLHCDTLGFFRSENKWNITSVIDHTGYI
DCKVCLLSNAKQRSKMHHSERKASRAHERLHCDTLGFRSENKWNITSVIDHTGYI
PSELNGLAEVUNKLLIQQIYRIVVTLGPQILKLITVVIQYSITMINHTFRRSLKGQT
PYSPLULSEGNFYFFFFAIDCVVTFENALERNYGVTSTKOAPBEIMENLIGKABDL
GYEVRGTYVESEYDNTHDVMHHSKISYEVUPAGPFLTTGNSSNEVINDDFUQITIEN
PYSVYLLKNNRCDIILSPNVRIURSTEVINSYLKNLGTTPMSHIVMAPGIQGRQSGA
PSYYVLLKNNRCDIILSPNVRIURSTEVINGTLTGNYSKFFVINDDFUQITIEN
TUSEDWHTSDYPERSAPDEQNPSLSANIGHVTEKIDEGNIBPSGDDDSVVINGNV
EGINVFKDABSIOGRUHKRSPSTAQVGLSHGPCGTFRSEESLASGTDHGVDIVKK
TUSEDWHTSDYPERSAPDEQNPSLSANIGHVTEKIDEGNIBPSGDDDSVVINGNV
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TUSEDWHTSDYPERSAPDEQNSSLSANIGHVTEKIDGRAFAHAVAADSFPLINGLDDHTELA
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1587..1661
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3661..3671 misc (enture

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6342 . . 6352 misc featuro

/noto="polypurine tract l' 6353 . . 6632

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ORIGIN

6633.,6637 /notes=3' target site duplication= 1121 c 1338 g 2074 c 1 estabatest tenategtt qtatettesa sesecgocas atsaggeet tetasaggest
61 Battagtgtt tecastest tectasces gtetasces gtetastggg atcastest
121 teragtgt tecastest gtetasces gtetasces gtetasgtat acadecasa casaccas RASE COUNT 121 taragegrig tergalacae grofabruge gebadaguat quacaegnad tamangustu 181 agaaaababa atmactaagg gadaquight ggreegigda clattrigeg teaglabacig 241 beebargaaa Rigatggrib Elaryagaat ggaaantiit toobtcacae atcaggrigat 491 BECHNEGHAN HEGNEGHELN CERTHOGNAT HEGNARDLE TOOREGACH ACCAMETAL
301 GREAGHACTA ACCATACITY EQUATIONS ENTRACES GREAGHAN ACCECAGES
361 LICCASCHA ALBRANGHA GEOLUCIC ENTRACE GROCONTOLO GREAGHAN AGLECGUECE
421 DETERMENT ACAMETAL ACCATACITY ACCATACA BECHNEGE ACCATACACTA ACCATACACTACACTA ACCATACACTA ACCATACACTACA 481 doarcagart agaagtogat agratare attreeted agartage tetranatt to agreece attreete training to agartage training to agartage training tra 481 doalcagatt agaagtogat agtgataatc attlegtedd aaattagegt tgtataaatt 1264 Catgoolcat actactcoan giggations goldacoang atscatcagt actectage 1321 Egeteraca tagetgaaga aatgtgtgar catectgatt argeragate ggttgacatt 1381 Egocorbeca tagergaago taaterratt ettagrera agascetgaa abaseasa 1381 egocorbeca sarargaaco taaterratt ettagrera engorbecaga gaaacondaa 1381 egocorbeca sarargaaco taaterratt ettagrera engorbecaga gaaacondaa 1381 egocorbeca tagergaago taaterratt ettagrera agascetgaa aberaagaag 1501 agabataaga aacarceasa arcagataac geraaanya agaarcegas accaagasag 1501 agabataaga aacarceasa arcagataac geraaagga aasaganaa agaasatacaa 1621 aactgoagaa aacarceasa arcagataac geraaanya agaarcegas accaagasag 1681 Startgaatt trassosttt aaggetraac sagtaretse tgratgatac rggrgccaca AND ACCOCCRATE GERROGERS ECCENTRATES SAFECTARES REGRESSES CREEKEST 2461 CONSTRUCTOR ARRESTS FOR ARRESTS CREEKEST GERROGERS ARRESTS GERRITARIS LOCALIZATION ARRESTS ACCORDED ARRESTS FOR ARRESTS ARREST ARRESTS ARRESTS ARRESTS ARRESTS ARRESTS ARRESTS ARRESTS ARRESTS 2641 Eggaalbate ggtttaaoga taaggtggee tacttcagee gtgalbatge tcotgagtto 2641 rggaaraate ggttraaga taaggtggca tactteaga grgaraatge tectgagrte
2701 coacaacert etgatriage tgagtteage arteggagg agacratage ggetraceg
2701 cocaacert atggetege cagagright aatsaatiga fricacaace gatrraceg
2821 atggetegg coacertage coacagreest taagtegatri attacgtgat reaginger
2881 arracaarga coacacace cocacgreest taagtegatri attacgtgat taagtegatri atggetegat taagtegatri atggetegat taagtegatri atggetegat taagtegatri atggetegat taagtegatri atggetegat taagtegatri atggetegatri atggeteg 3001 acattragta atgreatega anagnaregt tenggagura catcaactaa aggageteet JUNI BENEFERAÇÃO RESPONTES ANAGRANCIS LANGUAGELA CALEGRESA CALEGRESA ANGUAGELAS LA CONTRACTOR ACCORDANCE CARACTERA CALEGRESA CALEGRESA ANGUAGELAS CALEGRESA CALEGRESA ANGUAGELAS CALEGRESA C 3481 BOLGSFARE CYCLOSTER CALCACTOR GENERALES STEAMBERC ENFOCACE 3501 creacade tasadaste fassasted artsasses aracasada odeoceroc 3961 abccomance theasemanc contestes acadagate constants 4021 gacgaagtee crossquage aspaceacht astgaacaas cogatacagt tgatactgtt 1021 quequagres decampages ambanestes acemetants cattaganga tontarteas 4141 detectacas actograma estaganant scancagant conscitos attaganan cattaganant 4201 gazatetca cagtagetaa espaganant actualmenta tecamanan cattaganant Received Time 1930. Apr. 1918: 38 miras/query/cgl/scmdaffatilove&dbanucleoiida&iiaLulda=2273718&6001-

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Revised: October 24, 2001.

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